

Article

Supplementary file: Screening of a Novel Glycoside Hydrolase Family 51 α -L-arabinofuranosidase from *Paenibacillus polymyxa* KF-1: Cloning, Expression and Characterization

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Table S1. Other carbohydrate degrading enzymes identified by LC-MS/MS from *P. polymyxa*.

Entry name (Uniprot)	Accession No.	Protein description ¹	Signal peptide ²	Non-classical Signal ³	Family	Predicted Mw (kDa) ⁴	Predicted pI ⁴
E3EEC5	WP_013369681.1	glucanase	1-39		CBM3-GH6	77.017	5.51
E3E469	WP_013371213.1	β -glucanase	1-25		GH16	26.979	6.82
E3E5P0	WP_013372496.1	1,4- β -glucanase	1-32		GH5	44.467	5.68
E3E4B5	WP_013371259.1	endoglucanase	1-30		GH5	50.11	6.41
E0RJL4	WP_080942818.1	glucanase	1-39		CBM3-GH6	77.088	5.62
E3EJF1	WP_013371106.1	cellulose 1,4- β -cellobiosidase	1-38		CBM3-GH48	110.36	5.48
E0RLD5	ADM70135.2	cellulose 1,4- β -cellobiosidase	NO	YES	CBM3-GH48	113.23	5.77
E3E9Z4	WP_013372699.1	β -glucosidase	NO	NO	GH1	51.749	5.11
E3EC08	WP_013373881.1	cellulase	1-29		CBM_X2-GH5	63.43	6.96
E3EDF5	WP_013369567.1	pectate lyase	1-33		-	24.619	9.19
E3EEN8	WP_013370345.1	pectate lyase[1]	1-33		PL10	45.24	9.41
E3E7F9	WP_013373703.1	pectate lyase	1-34		PL9	46.988	5.50
E0RB75	WP_013308307.1	pectate lyase	1-32		PL1	72.777	6.18
E3EDI7	CCC83843.1	rhamnogalacturonate lyase	1-30		PL11	67.53	5.32
E3ED00	WP_013369503.1	endo- α -(1-5)-L-arabinanase	1-35		GH43	35.449	9.17
E0RHQ6	WP_013308827.1	endo- α -(1-5)-L-arabinanase	1-36		GH43	35.433	9.16
E3EJ95	WP_013370987.1	esterase	1-30		-	41.637	5.74
E3E5N6	WP_013372492.1	esterase	NO	NO	-	17.253	5.83
E3EAQ2	WP_013373348.1	glycoside hydrolase	1-27		-	40.047	4.95
E3ECI5	WP_013368970.1	glycoside hydrolase	1-27		GH43	88.171	5.75
E3EJJ5	WP_013371149.1	glycoside hydrolase	1-36		CBM59-GH5	53.518	5.99
E3EAR4	WP_017428602.1	glycoside hydrolase	NO	NO	-	24.379	5.26
E3EHP9	WP_013370917.1	glycoside hydrolase	NO	NO	-	70.846	5.43
E0REC8	WP_013312045.1	glycoside hydrolase family 81	1-24		CBM56-GH81	105.49	5.72
E0RHJ9	WP_013312241.1	glycoside hydrolase	1-27		-	38.63	4.89

¹Protein function was predicted by NCBI Blastp.

²Signal peptide was predicted by SignalP 4.1 server [2].

³Non-classical signal was predicted by SecretomeP 2.0 server [3].

⁴Molecular weight and pI were predicted by ExPASy- Compute pI/Mw tool [4].

Table S2. Other hemicellulase encoding genes identified by *P. polymyxa* genome.

Accession No.	Family	Signal peptide ¹	Protein description	Length
WP_013371974.1	GH43	No	β -xylosidase	525
WP_013368970.1	GH43	1-27	glycoside hydrolase	811
WP_013370550.1	GH43	No	β -xylosidase	461
CCC84702.1	GH43	No	α -N-arabinofuranosidase	323
WP_013373660.1	GH43	No	glycoside hydrolase	238
WP_013368899.1	GH51	No	α -L-arabinofuranosidase	1246

¹Signal peptide was predicted by SignalP 4.1 server [2].

References

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